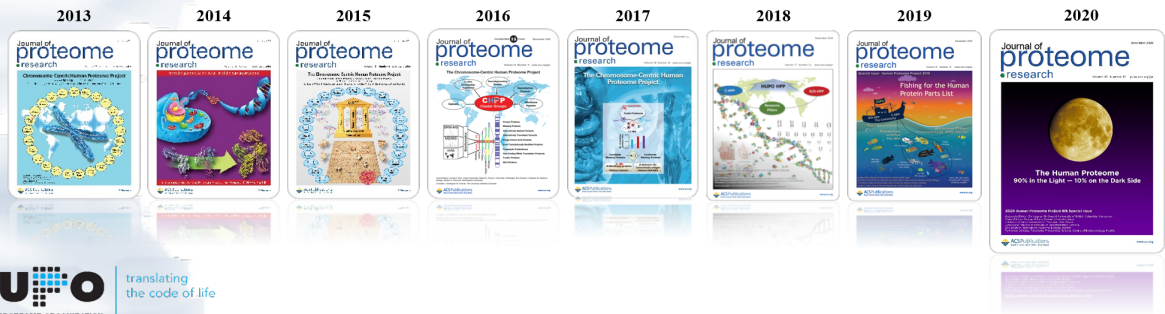


2021 JPR Special Issue Call for Papers

Submission Deadline: **June 30th, 2021**



The *Journal of Proteome Research* will publish its ninth annual Special Issue dedicated to highlighting the progress made on the HUPO Human Proteome Project (HPP). Since 2013, these Special Issues have captured incredibly important discoveries in the field, publishing over 250 articles that have collectively received over 5,000 citations. The Special Issue considers research papers encompassing both the Chromosome-Centric Human Proteome Project (C-HPP) and the Biology and Disease Human Proteome Project (B/D-HPP), as well from the Resource Pillars (Antibody, MS, Pathology, and Knowledgebase), and short definitive reports, submitted in the *Letters* format, on the discovery of a Missing Protein(s). To be considered, the missing protein(s) must meet the Guidelines v 3.0 and be cast in the context of the HPP and biological setting in which they were discovered.

Guest Editors

Young-Ki Paik, *Yonsei University*
Eric Deutsch, *Institute for Systems Biology*
Fernando Corrales, *CSIC, Madrid*
Lydie Lane, *Swiss Institute of Bioinformatics*
Gilbert S. Omenn, *University of Michigan*
Robert Moritz, *Institute for Systems Biology*

Associate Editor

Christopher M. Overall, *The University of British Columbia*

Thematic Priorities:

- Completing the high-resolution draft of the human proteome with new strategies and results leading to confident identifications of neXtProt missing proteins (PE2 – 4) according to the C-HPP Guidelines v 3.0 or recent updates
- Progress on the protein list of individual chromosomes and groups of chromosomes, annotating known proteins and their isoforms/proteoforms and/or credibly identifying missing proteins (PE2 – 4)
- Annotating proteins and their isoforms/proteoforms and/or identifying missing proteins found in rare or under explored cells and tissues, and protein lists of human cell types
- Produce and utilize “popular proteins” lists in B/D-HPP and contribute to the identification of missing proteins
- Proteomic studies of proteoforms produced by proteolytic processing, PTMs, alternative splicing (ASV), coding non-synonymous single nucleotide polymorphisms (cSNPs), or chromosome abnormalities
- Use of targeted proteomics, especially SRM and MS-SWATH, to extend chromosome-based protein findings
- New bioinformatic tools and approaches for annotating the human proteome
- Biological mechanistic analyses inspired from proteomics data in diseases or biological processes
- Biomarker discoveries based on the identification of novel ASVs, PTMs or cSNPs in proteomic studies
- Studies utilizing the Human Protein Atlas to identify missing proteins

Submission Procedure

Manuscripts must be submitted by 30th June, 2021 to be considered for this Special Issue. Manuscripts must be submitted electronically through the ACS Paragon Plus Environment online submission system. Specify in the authors' cover letter that the manuscript is intended for the HPP Special Issue.

Review and Publication Process

Editorial triage will determine whether manuscripts are appropriate for the HPP Special Issue, fulfill the HPP Guidelines 3.0 (2019-10-15) checklist (https://hupo.org/resources/Documents/HPPMSDataGuidelines_3.0.0.pdf) and protein evidence based on the 2021-02-18 neXtProt (<https://www.nextprot.org/about/protein-existence>) release to be considered for publication. The completed checklist *must* be included with the cover letter. The full MS data submission to ProteomeXchange *must* also be completed prior to initial submission, and the PXD number provided in the abstract. Nonconforming papers will be returned unreviewed. All relevant papers will go through full peer review. On acceptance papers will go online and be available in time for HUPO-2021. Due to the publication schedule, only papers that are accepted by September 31, 2021 will be published in the December 2021 HPP Special Issue. Papers requiring more time for revision or falling outside of the scope of the Special Issue will be published in regular issues of the Journal.

HPP Data Guidelines

Papers must conform to both the *Journal of Proteome Research* mass spectrometry guidelines and the HPP guidelines v 3.0 (see Deutsch *et al.* *J Proteome Res* 18, 4,108 – 4,116. doi.org/10.1021/acs.jproteome.9b00542 in order to be sent to review and for acceptance. All papers must analyze their data using the [Human PeptideAtlas](#) release 2021-02-11 and [neXtProt](#) release 2021-02-28. Papers not doing so will be returned without review.

